

SEQUENCE LISTING

<110> Kharbanda, Surrender
Kufe, Donald

<120> Modulation of Interaction of MUC1 with MUC1 Ligands

<130> DFCI:005US

<140> Unknown
<141> 2006-04-24

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<141> 2004-10-21

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<151> 2003-10-24

<150> 60/519,822
<151> 2003-11-12

<160> 71

<170> PatentIn version 3.3

<210> 1
<211> 164
<212> PRT
<213> Homo sapiens

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Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Thr
1 5 10 15

Val Leu Thr Ala Thr Thr Ala Pro Lys Pro Ala Thr Val Val Thr Gly
20 25 30

Ser Gly His Ala Ser Ser Thr Pro Gly Gly Glu Lys Glu Thr Ser Ala
35 40 45

Thr Gln Arg Ser Ser Val Pro Ser Ser Thr Glu Lys Asn Ala Phe Asn
50 55 60

Ser Ser Leu Glu Asp Pro Ser Thr Asp Tyr Tyr Gln Glu Leu Gln Arg
65 70 75 80

Asp Ile Ser Glu Met Phe Leu Gln Ile Tyr Lys Gln Gly Gly Phe Leu
85 90 95

Gly Leu Ser Asn Ile Lys Phe Arg Pro Gly Ser Val Val Val Gln Leu
100 105 110

Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp Met Glu Thr
115 120 125

Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr
130 135 140

Ile Ser Asp Val Ser Val Ser Asp Val Pro Phe Pro Phe Ser Ala Gln
145 150 155 160

Ser Gly Ala Gly

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<213> Homo sapiens

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480
492

<210> 3
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<212> PRT
<213> Homo sapiens

<400> 3

Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Thr
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Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
20 25 30

Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
35 40 45

Thr Glu Lys Asn Ala Phe Asn Ser Ser Leu Glu Asp Pro Ser Thr Asp
50 55 60

Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met Phe Leu Gln Ile
65 70 75 80

Tyr Lys Gln Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg Pro
85 90 95

Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile
100 105 110

Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala
115 120 125

Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val
130 135 140

Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala Gly
145 150 155

<210> 4
<211> 465
<212> DNA
<213> Homo sapiens

<400> 4
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<210> 5
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<213> Homo sapiens

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Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Thr
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Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
20 25 30

Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
35 40 45

Thr Glu Lys Asn Ala Leu Ser Thr Gly Val Ser Phe Phe Leu Ser
50 55 60

Phe His Ile Ser Asn Leu Gln Phe Asn Ser Ser Leu Glu Asp Pro Ser
65 70 75 80

Thr Asp Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met Phe Leu
85 90 95

Gln Ile Tyr Lys Gln Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe
100 105 110

Arg Pro Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly
115 120 125

Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr
130 135 140

Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser
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Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala Gly
165 170

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<212> DNA
<213> Homo sapiens

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cagagaagtt cagtccccag ctctactgag aagaatgctc tgtctactgg ggtctcttc 180
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accgactact accaagagct gcagagagac atttctgaaa tgttttgca gatttataaa 300
caaggggtt ttctggcct ctccaatatt aagttcaggc caggatctgt ggtggtacaa 360
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<213> Homo sapiens

<400> 7

Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Thr
1 5 10 15

Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
20 25 30

Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Thr
35 40 45

Asp Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met Phe Leu Gln
50 55 60

Ile Tyr Lys Gln Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg
65 70 75 80

Pro Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr
85 90 95

Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu
100 105 110

Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp
115 120 125

Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala Gly
130 135 140

<210> 8
<211> 420
<212> DNA
<213> Homo sapiens

<400> 8
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cagagaagtt cagtccccag caccgactac taccaagagc tgcagagaga catttctgaa 180
atgttttgc agatttataa acaaggggtt tttctgggcc tctccaatat taagttcagg 240
ccaggatctg tggtggtaca attgactctg gccttccgag aaggtaccat caatgtccac 300
gacatggaga cacagttcaa tcagtataaa acggaagcag cctctcgata taacctgacg 360
atctcagacg tcagcgtgag tgatgtgcca tttcctttct ctgcccagtc tggggctggg 420

<210> 9
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<212> PRT
<213> Homo sapiens

<400> 9

Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Thr
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Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
20 25 30

Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
35 40 45

Thr Glu Lys Asn Ala Ile Pro Ala Pro Thr Thr Lys Ser Cys Arg
50 55 60

Glu Thr Phe Leu Lys Trp Pro Gly Ser Val Val Gln Leu Thr Leu
65 70 75 80

Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp Val Glu Thr Gln Phe
85 90 95

Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser
100 105 110

Asp Val Ser Val Ser Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly
115 120 125

Ala Gly
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<210> 10
<211> 390
<212> DNA
<213> Homo sapiens

<400> 10
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cagagaagtt cagtccccag ctctactgag aagaatgcta tcccagcacc gactactacc 180
aagagctgca gagagacatt tctgaaatgg ccaggatctg tggtggtaca attgactctg 240
gccttccgag aaggtaccat caatgtccac gacatggaga cacagttcaa tcagtataaa 300
acggaagcag cctctcgata taacctgacg atctcagacg tcagcgtgag tcatgtgcca 360
tttcctttct ctgcccagtc tggggctggg 390

<210> 11
<211> 102
<212> PRT
<213> Homo sapiens

<400> 11

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6

Gln Arg Asp Ile Ser Glu Met Phe Leu Gln Ile Tyr Lys Gln Gly Gly
20 25 30

Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg Pro Gly Ser Val Val Val
35 40 45

Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp Val
50 55 60

Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr Asn
65 70 75 80

Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val Pro Phe Pro Phe Ser
85 90 95

Ala Gln Ser Gly Ala Gly
100

<210> 12

<211> 306

<212> DNA

<213> Homo sapiens

<400> 12

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ttcaggccag gatctgtggt ggtacaattt actctggcct tccgagaagg taccatcaat 180

gtccacgaca tggagacaca gttcaatcag tataaaacgg aagcagcctc tcgatataac 240

ctgacgatct cagacgtcag cgtgagtgat gtgccatttc ctttctctgc ccagtctggg 300

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<210> 13

<211> 375

<212> PRT

<213> Homo sapiens

<400> 13

Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Thr
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Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
20 25 30

Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
35 40 45

Thr Glu Lys Asn Ala Val Ser Met Thr Ser Ser Val Leu Ser Ser His
50 55 60

Ser Pro Gly Ser Gly Ser Ser Thr Thr Gln Gly Gln Asp Val Thr Leu
65 70 75 80

Ala Pro Ala Thr Glu Pro Ala Ser Gly Ser Ala Ala Thr Trp Gly Gln
85 90 95

Asp Val Thr Ser Val Pro Val Thr Arg Pro Ala Leu Gly Ser Thr Thr
100 105 110

Pro Pro Ala His Asp Val Thr Ser Ala Pro Asp Asn Lys Pro Ala Pro
115 120 125

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
130 135 140

Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
145 150 155 160

Ala Pro Asp Asn Arg Pro Ala Leu Gly Ser Thr Ala Pro Pro Val His
165 170 175

Asn Val Thr Ser Ala Ser Gly Ser Ala Ser Gly Ser Ala Ser Thr Leu
180 185 190

Val His Asn Gly Thr Ser Ala Arg Ala Thr Thr Thr Pro Ala Ser Lys
195 200 205

Ser Thr Pro Phe Ser Ile Pro Ser His His Ser Asp Thr Pro Thr Thr
210 215 220

Leu Ala Ser His Ser Thr Lys Thr Asp Ala Ser Ser Thr His His Ser
225 230 235 240

Thr Val Pro Pro Leu Thr Ser Ser Asn His Ser Thr Ser Pro Gln Leu
245 250 255

Ser Thr Gly Val Ser Phe Phe Leu Ser Phe His Ile Ser Asn Leu
260 265 270

Gln Phe Asn Ser Ser Leu Glu Asp Pro Ser Thr Asp Tyr Tyr Gln Glu
275 280 285

Leu Gln Arg Asp Ile Ser Glu Met Phe Leu Gln Ile Tyr Lys Gln Gly
290 295 300

Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg Pro Gly Ser Val Val
305 310 315 320

Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp
325 330 335

Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr
340 345 350

Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val Pro Phe Pro Phe
355 360 365

Ser Ala Gln Ser Gly Ala Gly
370 375

<210> 14
<211> 1125
<212> DNA
<213> Homo sapiens

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cagagaagtt cagtgcccag ctctactgag aagaatgctg tgagtatgac cagcagcgta 180
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acggtaacctc ctctcacctc ctccaatcac agcaattctc cccagttgtc tactggggtc 780
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ttcaatcagt ataaaacgga agcagcctct cgtatataacc tgacgatctc agacgtcagc 1080
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<210> 15
<211> 337
<212> PRT
<213> Homo sapiens

<400> 15

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Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
20 25 30

Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
35 40 45

Thr Glu Lys Asn Ala Val Ser Met Thr Ser Ser Val Leu Ser Ser His
50 55 60

Ser Pro Gly Ser Gly Ser Ser Thr Thr Gln Gly Gln Asp Val Thr Leu
65 70 75 80

Ala Pro Ala Thr Glu Pro Ala Ser Gly Ser Ala Ala Thr Trp Gly Gln
85 90 95

Asp Val Thr Ser Val Pro Val Thr Arg Pro Ala Leu Gly Ser Thr Thr
100 105 110

Pro Pro Ala His Asp Val Thr Ser Ala Pro Asp Asn Lys Asn Arg Pro
115 120 125

Ala Leu Gly Ser Thr Ala Pro Pro Val His Asn Val Thr Ser Ala Ser
130 135 140

Gly Ser Ala Ser Gly Ser Ala Ser Thr Leu Val His Asn Gly Thr Ser
145 150 155 160

Ala Arg Ala Thr Thr Thr Pro Ala Ser Lys Ser Thr Pro Phe Ser Ile
165 170 175

Pro Ser His His Ser Asp Thr Pro Thr Thr Leu Ala Ser His Ser Thr
180 185 190

Lys Thr Asp Ala Ser Ser Thr His His Ser Thr Val Pro Pro Leu Thr
195 200 205

Ser Ser Asn His Ser Thr Ser Pro Gln Leu Ser Thr Gly Val Ser Phe
210 215 220

Phe Phe Leu Ser Phe His Ile Ser Asn Leu Gln Phe Asn Ser Ser Leu
225 230 235 240

Glu Asp Pro Ser Thr Asp Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser
245 250 255

Glu Met Phe Leu Gln Ile Tyr Lys Gln Gly Gly Phe Leu Gly Leu Ser
260 265 270

Asn Ile Lys Phe Arg Pro Gly Ser Val Val Val Gln Leu Thr Leu Ala
275 280 285

Phe Arg Glu Gly Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn
290 295 300

Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp
305 310 315 320

Val Ser Val Ser Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala
325 330 335

Gly

<210> 16
<211> 1011
<212> DNA
<213> Homo sapiens

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cagagaagtt cagtccccag ctctactgag aagaatgctg tgagtatgac cagcagcgta 180
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gaagatccca gcaccgacta ctaccaagag ctgcagagag acatttctga aatgttttg 780

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<210> 17
<211> 175
<212> PRT
<213> Homo sapiens

<400> 17

Ala Thr Thr Thr Pro Ala Ser Lys Ser Thr Pro Phe Ser Ile Pro Ser
1 5 10 15

His His Ser Asp Thr Pro Thr Thr Leu Ala Ser His Ser Thr Lys Thr
20 25 30

Asp Ala Ser Ser Thr His His Ser Thr Val Pro Pro Leu Thr Ser Ser
35 40 45

Asn His Ser Thr Ser Pro Gln Leu Ser Thr Gly Val Ser Phe Phe Phe
50 55 60

Leu Ser Phe His Ile Ser Asn Leu Gln Phe Asn Ser Ser Leu Glu Asp
65 70 75 80

Pro Ser Thr Asp Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met
85 90 95

Phe Leu Gln Ile Tyr Lys Gln Gly Gly Phe Leu Gly Leu Ser Asn Ile
100 105 110

Lys Phe Arg Pro Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg
115 120 125

Glu Gly Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr
130 135 140

Lys Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser
145 150 155 160

Val Ser Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala Gly
165 170 175

<210> 18
<211> 525
<212> DNA
<213> Homo sapiens

<400> 18
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acggtacctc ctctcacctc ctccaatcac agcacttctc cccagttgtc tactgggtc 180
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<210> 19

<211> 58

<212> PRT

<213> Homo sapiens

<400> 19

Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn
1 5 10 15

Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala
20 25 30

Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val Pro
35 40 45

Phe Pro Phe Ser Ala Gln Ser Gly Ala Gly
50 55

<210> 20

<211> 174

<212> DNA

<213> Homo sapiens

<400> 20

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gacgtcagcg tgagtgatgt gccatttcct ttctctgccccc agtctggggc tggg 174

<210> 21

<211> 50

<212> PRT

<213> Homo sapiens

<400> 21

Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn
1 5 10 15

Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala
20 25 30

Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val Pro
35 40 45

Phe Pro
50

<210> 22
<211> 150
<212> DNA
<213> Homo sapiens

<400> 22
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gacgtcagcg tgagtgtatgt gccatttcct 150

<210> 23
<211> 49
<212> PRT
<213> Homo sapiens

<400> 23

Phe Arg Glu Gly Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn
1 5 10 15

Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp
20 25 30

Val Ser Val Ser Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala
35 40 45

Gly

<210> 24
<211> 147
<212> DNA
<213> Homo sapiens

<400> 24
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cctttctctg cccagtctgg ggctggg 147

<210> 25
<211> 120
<212> PRT
<213> Homo sapiens

<400> 25

Leu Ser Thr Gly Val Ser Phe Phe Phe Leu Ser Phe His Ile Ser Asn
1 5 10 15

Leu Gln Phe Asn Ser Ser Leu Glu Asp Pro Ser Thr Asp Tyr Tyr Gln
20 25 30

Glu Leu Gln Arg Asp Ile Ser Glu Met Phe Leu Gln Ile Tyr Lys Gln
35 40 45

Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg Pro Gly Ser Val
50 55 60

Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His
65 70 75 80

Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg
85 90 95

Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val Pro Phe Pro
100 105 110

Phe Ser Ala Gln Ser Gly Ala Gly
115 120

<210> 26
<211> 360
<212> DNA
<213> Homo sapiens

<400> 26
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ccaggatctg tgggtgtaca attgactctg gccttccgag aaggtaccat caatgtccac 240
gacatggaga cacagttcaa tcagtataaa acggaagcag cctctcgata taacctgacg 300
atctcagacg tcagcgtgag tggatgtgcca tttcccttct ctgcccagtc tggggctggg 360

<210> 27
<211> 77
<212> PRT
<213> Homo sapiens

<400> 27

Ile Pro Ala Pro Thr Thr Thr Lys Ser Cys Arg Glu Thr Phe Leu Lys
1 5 10 15

Trp Pro Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly
20 25 30

Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr
35 40 45

Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser
50 55 60

Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala Gly
65 70 75

<210> 28

<211> 231

<212> DNA

<213> Homo sapiens

<400> 28

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acacagttca atcagtataa aacggaagca gcctctcgat ataacctgac gatctcagac 180

gtcagcgtga gtgatgtgcc atttccttcc tctgcccagt ctggggctgg g 231

<210> 29

<211> 112

<212> PRT

<213> Homo sapiens

<400> 29

Leu Ser Thr Gly Val Ser Phe Phe Phe Leu Ser Phe His Ile Ser Asn
1 5 10 15

Leu Gln Phe Asn Ser Ser Leu Glu Asp Pro Ser Thr Asp Tyr Tyr Gln
20 25 30

Glu Leu Gln Arg Asp Ile Ser Glu Met Phe Leu Gln Ile Tyr Lys Gln
35 40 45

Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg Pro Gly Ser Val
50 55 60

Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His
65 70 75 80

Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg
85 90 95

Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val Pro Phe Pro
100 105 110

<210> 30
<211> 336
<212> DNA
<213> Homo sapiens

<400> 30
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atgttttgc agatttataa acaagggggt tttctgggcc tctccaatat taagttcagg 180
ccaggatctg tgggtgtaca attgactctg gccttccgag aaggtaccat caatgtccac 240
gacatggaga cacagttcaa tcagtataaa acggaagcag cctctcgata taacctgacg 300
atctcagacg tcagcgtgag tggatgtgcca tttcct 336

<210> 31
<211> 66
<212> PRT
<213> Homo sapiens

<400> 31

Ile Pro Ala Pro Thr Thr Lys Ser Cys Arg Glu Thr Phe Leu Lys
1 5 10 15

Trp Pro Gly Ser Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly
20 25 30

Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr
35 40 45

Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser
50 55 60

Asp Val
65

<210> 32
<211> 198
<212> DNA
<213> Homo sapiens

<400> 32
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gtgggtgtac aattgactct ggccttccga gaaggtacca tcaatgtcca cgacatggag 120

acacagttca atcagtataa aacggaagca gcctctcgat ataacctgac gatctcagac 180
gtcagcgtga gtgatgtg 198

<210> 33
<211> 232
<212> PRT
<213> HS

<400> 33

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala
1 5 10 15

Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
20 25 30

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
35 40 45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
50 55 60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65 70 75 80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
85 90 95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
100 105 110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
115 120 125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
130 135 140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145 150 155 160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
165 170 175

Lys Thr Thr Pro Pro Val Leu Asp Ser Val Gly Ser Phe Phe Leu Tyr
180 185 190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
195 200 205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
210 215 220

Ser Leu Ser Leu Ser Pro Gly Lys
225 230

<210> 34
<211> 699
<212> DNA
<213> HS

<400> 34
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gggggaccgt cagtcttcct cttccccca aaacccaagg acaccctcat gatctcccgg 120
acccctgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc 180
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgca ggaggagcag 240
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat 300
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagccccat cgagaaaacc 360
atctccaaag ccaaaggca gccccgagaa ccacaggtgt acaccctgcc cccatcccg 420
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc 480
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct 540
cccgtgctgg actccgtcgg ctcctcttc ctctacagca agtcaccgt ggacaagagc 600
aggtggcagc agggAACgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac 660
tacacgcaga agagcctctc cctgtctccg ggtaaatga 699

<210> 35
<211> 230
<212> PRT
<213> HS

<400> 35

Lys Ser Cys Asp Lys Pro His Thr Cys Pro Leu Cys Pro Ala Pro Glu
1 5 10 15

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
20 25 30

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
35 40 45

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
50 55 60

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
65 70 75 80
19

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
85 90 95

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
100 105 110

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
115 120 125

Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
130 135 140

Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
145 150 155 160

Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Ala
165 170 175

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
180 185 190

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
195 200 205

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
210 215 220

Ser Leu Ser Pro Gly Lys
225 230

<210> 36
<211> 690
<212> DNA
<213> HS

<400> 36
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gaggtcacat gcgtgggtggt ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 180
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 240
agcacgtacc gtgtggtcag cgtccctcacc gtcctgcacc aggactggct gaatggcaag 300
gagtacaagt gcaaggcttc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 360
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgccccatc ccggatgag 420
ctgaccaaga accaggtcag cctgacactgc ctagtcaaag gcttctatcc cagcgacatc 480

gccgtggagt gggagagcaa tgggcagccg gagaacaact acaaggccac gcctcccg 540
ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcagg 600
cagcagggaa acgtttctc atgctccgtg atgcatgagg ctctgcacaa ccactacac 660
cagaagagcc tctccctgtc tccggtaaa 690

<210> 37
<211> 228
<212> PRT
<213> HS

<400> 37

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val
1 5 10 15

Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
20 25 30

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
35 40 45

His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Met Glu
50 55 60

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
65 70 75 80

Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn
85 90 95

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro
100 105 110

Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln
115 120 125

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
130 135 140

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145 150 155 160

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
165 170 175

Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
180 185 190

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
195 200 205

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
210 215 220

Ser Pro Gly Lys
225

<210> 38
<211> 687
<212> DNA
<213> HS

<400> 38
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acgtgcgtgg tggtggacgt gagccacgaa gaccccgagg tccagttcaa ctggtacgtg 180
gacggcatgg aggtgcataa tgccaagaca aagccacggg aggagcagtt caacagcacg 240
ttccgtgtgg tcagcgtcct caccgtcgtg caccaggact ggctgaacgg caaggagttac 300
aagtgcagg tctccaacaa aggcctccca gccccatcg agaaaaccat ctccaaaacc 360
aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccgga ggagatgacc 420
aagaaccagg tcagcctgac ctgcctggc aaaggcttct accccagcga catgcccgtg 480
gagtggaga gcaatggca gccggagaac aactacaaga ccacacctcc catgctggac 540
tccgacggct ccttcttcct ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 600
gggaacgtct tctcatgctc cgtgatgcat gaggctctgc acaaccacta cacacagaag 660
agcctctccc tgtctccggg taaatga 687

<210> 39
<211> 229
<212> PRT
<213> Homo Sapiens

<400> 39

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe
1 5 10 15

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
20 25 30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
50 55 60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
 65 70 75 80

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
 85 90 95

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
 100 105 110

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
 115 120 125

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
 130 135 140

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
 145 150 155 160

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
 165 170 175

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
 180 185 190

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
 195 200 205

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
 210 215 220

Leu Ser Leu Gly Lys
 225

<210> 40
 <211> 690
 <212> DNA
 <213> HS

<400> 40
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 gtcacgtgcg tggtggtgga cgtgagccag gaagaccccg aggtccagtt caactggtag 180
 gtggatggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gttcaacagc 240
 acgtaccgtg tggtcagcgt cctcaccgtc ctgcaccagg actggctgar cggcaaggag 300
 tacaagtgcg aggtctccar caaaggcctc ccgtcctcca tcgagaaaac catctccaa 360

gccccaggc	agccccgaga	gccacaggtg	tacaccctgc	ccccatccca	ggaggagatg	420
accaagaacc	aggtcagcct	gacctgcctg	gtcaaaggct	tctacccca	cgacatcgcc	480
gtggagtgg	agagcaatgg	gcagccggag	aacaactaca	agaccacgcc	tcccgtgctg	540
gactccgacg	gctccttctt	cctctacagc	aggctaaccg	tggacaagag	cagktggcag	600
gagggaaatg	tcttctcatg	ctccgtgatg	catgaggctc	tgcacaacca	ctacacacag	660
aagagcctct	ccctgtctct	gggtaaatga				690

<210>	41
<211>	585
<212>	PRT
<213>	HS
<400>	41

Asp	Ala	His	Lys	Ser	Glu	Val	Ala	His	Arg	Phe	Lys	Asp	Leu	Gly	Glu
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Glu	Asn	Phe	Lys	Ala	Leu	Val	Leu	Ile	Ala	Phe	Ala	Gln	Tyr	Leu	Gln
		20				25						30			

Gln	Cys	Pro	Phe	Glu	Asp	His	Val	Lys	Leu	Val	Asn	Glu	Val	Thr	Glu
		35				40					45				

Phe	Ala	Lys	Thr	Cys	Val	Ala	Asp	Glu	Ser	Ala	Glu	Asn	Cys	Asp	Lys
		50				55				60					

Ser	Leu	His	Thr	Leu	Phe	Gly	Asp	Lys	Leu	Cys	Thr	Val	Ala	Thr	Leu
		65			70				75			80			

Arg	Glu	Thr	Tyr	Gly	Glu	Met	Ala	Asp	Cys	Cys	Ala	Lys	Gln	Glu	Pro
		85			90						95				

Glu	Arg	Asn	Glu	Cys	Phe	Leu	Gln	His	Lys	Asp	Asp	Asn	Pro	Asn	Leu
						100		105				110			

Pro	Arg	Leu	Val	Arg	Pro	Glu	Val	Asp	Val	Met	Cys	Thr	Ala	Phe	His
		115				120				125					

Asp	Asn	Glu	Glu	Thr	Phe	Leu	Lys	Lys	Tyr	Leu	Tyr	Glu	Ile	Ala	Arg
		130				135				140					

Arg	His	Pro	Tyr	Phe	Tyr	Ala	Pro	Gln	Leu	Leu	Phe	Phe	Ala	Lys	Arg
		145			150				155			160			

Tyr	Lys	Ala	Ala	Phe	Thr	Glu	Cys	Cys	Gln	Ala	Ala	Asp	Lys	Ala	Ala
		165				170			175						

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
210 215 220

Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Pro Asp Pro His Glu
355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Met Glu Glu Pro
370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu
385 390 395 400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
580 585

<210> 42
<211> 1758
<212> DNA
<213> HS

<400> 42
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gccttggtgt tgattgcctt tgctcagtat cttcagcagt gtccatttga agatcatgtat
aaatttagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgtatga gtcagctgaa 120
aattgtgaca aatcacttca tacccaaaaat ggagacaaat tatgcacagt tgcaactctt
cgtgaaacct atggtaaat ggctgactgc tgtgcacaaac aagaacctga gagaaatgaa 180
tgcttcttgc aacacaaaga tgacaatcca aatctcccc gattggtgag accagaggat 240
gatgtatgt gcactgcttt tcatgacaat gaagagacat ttttggaaaa atacttataat
gaaattgcca gaagacatcc ttactttat gccccgcaac tcctttctt tgctaaaagg 300
tataaagctg ctttacaga atgttgccaa gctgctgata aagcagcctg cctgttgcca 360
540

aagctcgatg aacttcggga tgaagggaag gcttcgtctg ccaaacagag actcaagtgt	600
gccagtcctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc	660
cagagatttc ccaaagctga gtttgcagaa gtttccaagt tagtgcacaga tcttaccaa	720
gtccacacgg aatgctgcca tggagatctg cttgaatgtg ctgatgcacag ggcggacctt	780
gccaagtata tctgtgaaaaa tcaagattcg atctccagta aactgaagga atgctgtgaa	840
aaacctctgt tgaaaaatcc ccaactgcatt gccgaagtgg aaaatgtga gatgcctgct	900
gacttgcctt cattagcggc tgattttgtt gaaagtaagg atgttgcaa aaactatgct	960
gaggcaaagg atgtcttctt gggcatgttt ttgtatgaat atgcaagaag gcatcctgat	1020
tactctgtcg tactgctgct gagacttgcc aagacatatg aaaccactct agagaagtgc	1080
tgtgccgctc cagatcctca tgaatgctat gccaaagtgt tcgatgaatt taaaccttctt	1140
atggaagagc ctcagaattt aatcaaacaa aattgtgagc ttttgagca gcttggagag	1200
tacaaattcc agaatgcgct attagttcg taccaccaaga aagtacccca agtgtcaact	1260
ccaactcttg tagaggtctc aagaaaccta ggaaaagtgg gcagcaaatg ttgtaaacat	1320
cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtggcctt gaaccaggta	1380
tgtgtgttgc atgagaaaac gccagtaagt gacagagtca ccaaatgctg cacagaatcc	1440
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gagtttaatg ctgaaacatt caccttccat gcagatatat gcacacttgc tgagaaggag	1560
agacaaatca agaaacaaac tgcacttgc gagcttgc aacacaagcc caaggcaaca	1620
aaagagcaac tgaagctgt tatggatgat ttgcagctt ttgtagagaa gtgctgcaag	1680
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gctgccttag gcttataa	1758

<210> 43
 <211> 110
 <212> PRT
 <213> Homo Sapiens

<400> 43

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Val Cys Ala Tyr Asp Pro Glu Ala Ala Ser Ala Pro Gly Ser Gly Asn
 20 25 30

Pro Cys His Glu Ala Ser Ala Ala Gln Lys Glu Asn Ala Gly Glu Asp
 35 40 45

Pro Gly Leu Ala Arg Gln Ala Pro Lys Pro Arg Lys Gln Arg Ser Ser
 50 55 60

Leu Leu Glu Lys Gly Leu Asp Gly Ala Lys Lys Ala Val Gly Gly Leu
65 70 75 80

Gly Lys Leu Gly Lys Asp Ala Val Glu Asp Leu Glu Ser Val Gly Lys
85 90 95

Gly Ala Val His Asp Val Lys Asp Val Leu Asp Ser Val Leu
100 105 110

<210> 44
<211> 333
<212> DNA
<213> HS

<400> 44
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caaaaaggaaa atgcaggtga agacccaggg ttagccagac aggcaccaaa gccaaggaag 180
cagagatcca gccttctgga aaaaggccta gacggagcaa aaaaagctgt ggggggactc 240
ggaaaactag gaaaagatgc agtcgaagat ctagaaagcg tgggtaaagg agccgtccat 300
gacgttaaag acgtccttga ctcagacta tag 333

<210> 45
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 45
aacccttgcc atgaaggcatc a 21

<210> 46
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 46
aagcatcagc agctcaaaaag g 21

<210> 47
<211> 21
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<220>
<223> Synthesized Sequence

<400> 47	21
aaaaggaaaa tgcaaggtaa g	
<210> 48	
<211> 21	
<212> DNA	
<213> Artificial	
<220>	
<223> Synthesized Sequence	
<400> 48	21
aaaggaaaaat gcaggtaaag a	
<210> 49	
<211> 21	
<212> DNA	
<213> Artificial	
<220>	
<223> Synthesized Sequence	
<400> 49	21
aaggaaaaatg caggtaaaga c	
<210> 50	
<211> 21	
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<223> Synthesized Sequence	
<400> 50	21
aaaatgcagg tgaagaccca g	
<210> 51	
<211> 21	
<212> DNA	
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<400> 51	21
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<210> 52	
<211> 21	
<212> DNA	
<213> Artificial	
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<223> Synthesized Sequence	
<400> 52	21
aaagccaaagg aaggcagagat c	

<210> 53
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 53
aagccaagga agcagagatc c 21

<210> 54
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 54
aaggaaggcag agatccagcc t 21

<210> 55
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 55
aagcagagat ccagccttct g 21

<210> 56
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 56
aaaaaggcct agacggagca a 21

<210> 57
<211> 21
<212> DNA
<213> Artificial

<220>
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35 40 45

Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp Val
50 55 60

Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr Asn
65 70 75 80

Leu Thr Ile Ser Asp Val Ser Val Asp Val Pro Phe Pro Phe Ser
85 90 95

Ala Gln Ser Gly Ala Gly Lys Leu Lys Ser Cys Asp Lys Pro His Thr
100 105 110

Cys Pro Leu Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
115 120 125

Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
130 135 140

Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
145 150 155 160

Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
33

165

170

175

Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val
 180 185 190

Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
 195 200 205

Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
 210 215 220

Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
 225 230 235 240

Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
 245 250 255

Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly
 260 265 270

Gln Pro Glu Asn Asn Tyr Lys Ala Thr Pro Pro Val Leu Asp Ser Asp
 275 280 285

Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
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gtccacgaca tggagacaca gttcaatcag tataaaacgg aagcagcctc tcgatataac 240

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